

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 21, 2006, 23:30:26 ; Search time 196 Seconds

(without alignments)
11.664 Million cell updates/sec

Title: US-10-766-527-1

Perfect score: 31

Sequence: 1 YGFG3 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 300 summaries

Database :

A_Geneseq_8:*

- 1: Geneseq1980s:*
- 2: Geneseq1980s:*
- 3: Geneseq2000s:*
- 4: Geneseq2000s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*
- 9: Geneseq2005s:*
- 10: Geneseq2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	5	2	AAR76124 Osteogeni
2	31	100.0	5	2	ADC73222 Cyclic ps
3	31	100.0	5	6	ABP72525 Osteogeni
4	31	100.0	6	2	AAR62388 Osteoblas
5	31	100.0	6	2	AAR62954 Osteogeni
6	31	100.0	6	2	ADC73230 Cyclic ps
7	31	100.0	6	2	ADC73233 Cyclic ps
8	31	100.0	6	2	ADC73229 Cyclic ps
9	31	100.0	6	6	ABP72528 Osteogeni
10	31	100.0	6	8	ADU78752 Hemopole
11	31	100.0	6	8	ADU78752 Hemopole
12	31	100.0	14	2	AAR43890 Osteogeni
13	31	100.0	14	2	AAR43888 Osteogeni
14	31	100.0	14	2	AAR62952 Osteogeni
15	31	100.0	14	4	AAB92061 Growth fa
16	31	100.0	14	6	ABR63887 Osteogeni
17	31	100.0	14	6	ADA27392 Osteogeni
18	31	100.0	14	8	ADA27392 Osteogeni
19	31	100.0	14	9	AEC78137 Human OGP
20	31	100.0	14	9	AEC78137 Osteogeni
21	31	100.0	14	9	AED35403 Drug deli
22	31	100.0	14	9	AED61987 Osteogeni
23	31	100.0	17	2	AAR43889 Osteogeni
					AAR48440 Histogran

24	31	100.0	17	2	AAR48449 Histogran
25	31	100.0	17	2	AAR48442 Histogran
26	31	100.0	17	2	AAR48448 Histogran
27	31	100.0	17	2	AAR48444 Histogran
28	31	100.0	17	2	AAR48445 Histogran
29	31	100.0	17	2	AAR48450 Histogran
30	31	100.0	17	2	AAR48443 Histogran
31	31	100.0	17	2	AAR48447 Histogran
32	31	100.0	17	2	AAR48446 Histogran
33	31	100.0	17	2	AAR48441 Histogran
34	31	100.0	17	9	AED35422 Drug deli
35	31	100.0	17	9	AED35421 Drug deli
36	31	100.0	20	9	AED35418 Drug deli
37	31	100.0	20	9	AED35419 Drug deli
38	31	100.0	20	9	AED35420 Drug deli
39	31	100.0	21	9	AED61989 Osteogeni
40	31	100.0	35	9	AED61991 Osteogeni
41	31	100.0	90	4	AM17849 Peptide #
42	31	100.0	90	4	AB36867 Peptide #
43	31	100.0	90	4	AM30355 Peptide #
44	31	100.0	90	4	AB31654 Peptide #
45	31	100.0	90	4	AB22193 Protein #
46	31	100.0	90	4	AM570017 Human bon
47	31	100.0	90	4	AM57613 Human bra
48	31	100.0	90	4	AB31713 Human liv
49	31	100.0	90	4	AM05496 Peptide #
50	31	100.0	90	5	AB39647 Human pep
51	31	100.0	91	9	ADW17338 Eucalyptu
52	31	100.0	93	9	ADW17339 Eucalyptu
53	31	100.0	102	2	AY07283 Human his
54	31	100.0	102	2	AY07282 Histone H
55	31	100.0	102	2	AY05481 Human his
56	31	100.0	102	2	AY05480 Consensus
57	31	100.0	102	7	ADD45890 Rat Prote
58	31	100.0	102	7	AD60487 Human Pro
59	31	100.0	102	7	ADD45892 Human Pro
60	31	100.0	102	7	AD60485 Rat Prote
61	31	100.0	102	7	AD68426 Human his
62	31	100.0	102	7	AD68427 Human hea
63	31	100.0	102	8	ADP71922 Yeast wil
64	31	100.0	102	8	ADP71923 Yeast his
65	31	100.0	102	8	ADP71925 Yeast his
66	31	100.0	102	8	AD48808 Human his
67	31	100.0	102	8	ADT58370 Plant pol
68	31	100.0	102	9	AED66775 S. cerevi
69	31	100.0	103	3	AAG40967 Zea may
70	31	100.0	103	3	AAG08610 Arabidops
71	31	100.0	103	3	AAG54231 Arabidops
72	31	100.0	103	3	AAG44377 Arabidops
73	31	100.0	103	3	AAG26094 Zea may
74	31	100.0	103	3	AAG14777 Arabidops
75	31	100.0	103	3	AAG34651 Arabidops
76	31	100.0	103	3	AAG07684 Arabidops
77	31	100.0	103	3	AAG47837 Arabidops
78	31	100.0	103	3	AAG24508 Arabidops
79	31	100.0	103	3	AAG07997 Arabidops
80	31	100.0	103	3	AAG41091 Zea may
81	31	100.0	103	3	AAG49289 Arabidops
82	31	100.0	103	3	AAG37291 Arabidops
83	31	100.0	103	3	AAG21834 Arabidops
84	31	100.0	103	3	AAG54531 Zea may
85	31	100.0	103	3	AAG54656 Zea may
86	31	100.0	103	3	AAG15589 Arabidops
87	31	100.0	103	3	AAG40676 Zea may
88	31	100.0	103	3	AAG41424 Arabidops
89	31	100.0	103	3	AAG45956 Arabidops
90	31	100.0	103	3	AAG38702 Arabidops
91	31	100.0	103	3	AAG40899 Zea may
92	31	100.0	103	3	AAG05303 Arabidops
93	31	100.0	103	4	AB559852 Drosophi
94	31	100.0	103	4	AM78975 Human pro
95	31	100.0	103	5	AB93040 S. cerevi
96	31	100.0	103	5	AB93183 S. cerevi

STC sequence search results

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OM protein - protein search, using sw model

Run on: August 21, 2006, 23:39:22 ; Search time 52 Seconds
(without alignments)
8.416 Million cell updates/sec

Title: US-10-766-527-1

Perfect score: 31

Sequence: 1 YGFG 5

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 300 summaries

Database :

Issued Patents, AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/1aa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/1aa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/1aa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/1aa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/1aa/PTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/1aa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	5	1	US-08-530-277-1
2	31	100.0	5	2	US-09-150-621-4
3	31	100.0	5	2	US-09-150-621-6
4	31	100.0	5	2	US-09-150-621-7
5	31	100.0	5	2	US-09-150-621-8
6	31	100.0	5	2	US-09-150-621-9
7	31	100.0	5	2	US-09-150-621-10
8	31	100.0	5	2	US-09-150-621-27
9	31	100.0	5	2	US-09-150-621-32
10	31	100.0	5	2	US-09-150-621-35
11	31	100.0	5	2	US-09-150-621-47
12	31	100.0	5	2	US-09-150-621-48
13	31	100.0	5	2	US-09-150-621-49
14	31	100.0	5	2	US-09-150-621-50
15	31	100.0	5	2	US-09-150-621-51
16	31	100.0	5	2	US-09-150-621-61
17	31	100.0	6	1	US-08-530-277-6
18	31	100.0	6	2	US-09-150-621-38
19	31	100.0	6	2	US-09-150-621-39
20	31	100.0	6	2	US-09-150-621-40
21	31	100.0	6	2	US-09-150-621-41
22	31	100.0	6	2	US-09-150-621-53
23	31	100.0	6	2	US-09-150-621-59
24	31	100.0	10	7	5461034-5
25	31	100.0	11	7	5461034-4
26	31	100.0	12	7	5461034-3

27	31	100.0	13	7	5461034-2	Patent No. 5461034
28	31	100.0	14	1	US-08-530-277-4	Sequence 1, Appl
29	31	100.0	14	2	US-09-150-621-1	Sequence 1, Appl
30	31	100.0	14	2	US-09-150-621-54	Sequence 54, Appl
31	31	100.0	14	2	US-09-150-621-55	Sequence 55, Appl
32	31	100.0	14	2	US-09-623-548A-1237	Sequence 1237, Ap
33	31	100.0	14	2	US-09-657-276-1237	Sequence 1237, Ap
34	31	100.0	14	2	US-10-068-905-3	Sequence 3, Appl
35	31	100.0	14	7	5461034-1	Patent No. 5461034
36	31	100.0	15	2	US-09-530-123B-13	Sequence 13, Appl
37	31	100.0	15	2	US-10-437-435-13	Sequence 13, Appl
38	31	100.0	103	2	US-09-949-016-6380	Sequence 6380, Ap
39	31	100.0	103	2	US-09-949-016-6381	Sequence 6381, Ap
40	31	100.0	103	2	US-09-949-016-6382	Sequence 6382, Ap
41	31	100.0	103	2	US-09-949-016-6388	Sequence 6388, Ap
42	31	100.0	107	2	US-09-248-796A-18645	Sequence 18645, A
43	31	100.0	111	2	US-09-949-016-8136	Sequence 8136, Ap
44	31	100.0	115	2	US-09-248-796A-18646	Sequence 18646, A
45	31	100.0	120	2	US-09-949-016-8186	Sequence 8186, Ap
46	31	100.0	122	2	US-09-949-016-8157	Sequence 8157, Ap
47	31	100.0	141	2	US-09-949-016-8229	Sequence 8229, Ap
48	31	100.0	151	2	US-09-270-767-45274	Sequence 45274, A
49	31	100.0	213	2	US-09-252-991A-29929	Sequence 29929, A
50	31	100.0	220	2	US-09-902-540-12909	Sequence 12909, A
51	31	100.0	272	2	US-09-248-796A-21180	Sequence 21180, A
52	31	100.0	290	2	US-09-602-787A-670	Sequence 670, App
53	31	100.0	319	2	US-09-134-001C-3888	Sequence 3888, Ap
54	31	100.0	344	2	US-08-311-731A-82	Sequence 82, Appl
55	31	100.0	370	2	US-09-342-143-2	Sequence 2, Appl
56	31	100.0	370	2	US-09-924-439-2	Sequence 2935, Ap
57	31	100.0	372	2	US-09-540-236-2935	Sequence 16, Appl
58	31	100.0	417	2	US-09-710-262E-16	Sequence 2752, Ap
59	31	100.0	419	2	US-09-583-110-3752	Sequence 3756, Ap
60	31	100.0	425	2	US-09-107-433-3776	Sequence 15197, A
61	31	100.0	428	2	US-09-248-796A-15197	Sequence 2, Appl
62	31	100.0	465	2	US-08-788-231A-2	Sequence 2, Appl
63	31	100.0	465	2	US-09-495-239A-2	Sequence 4, Appl
64	31	100.0	465	2	US-09-043-944-4	Sequence 4, Appl
65	31	100.0	465	2	US-10-811-159-4	Sequence 1, Appl
66	31	100.0	546	1	US-09-067-351-1	Sequence 1, Appl
67	31	100.0	546	2	US-09-360-480-1	Sequence 6628, Ap
68	31	100.0	564	2	US-09-949-016-6628	Sequence 3772, Ap
69	31	100.0	567	2	US-10-104-047-3772	Sequence 11035, A
70	31	100.0	569	2	US-09-949-016-11035	Sequence 11036, A
71	31	100.0	569	2	US-09-949-016-11036	Sequence 4334, Ap
72	31	100.0	599	2	US-09-107-433-4334	Sequence 2449, Ap
73	31	100.0	967	2	US-09-540-246-2449	Sequence 6, Appl
74	31	100.0	974	2	US-08-960-048-6	Sequence 3366, Ap
75	31	100.0	974	2	US-09-838-586-6	Sequence 12, Appl
76	31	100.0	1032	1	US-09-583-110-3366	Sequence 28, Appl
77	31	100.0	1876	1	US-08-609-049A-12	Sequence 28, Appl
78	31	100.0	1876	2	US-08-609-049A-28	Sequence 28, Appl
79	31	100.0	1876	2	US-09-170-996-12	Sequence 28, Appl
80	31	100.0	1876	2	US-09-170-996-28	Sequence 4, Appl
81	31	100.0	24	2	US-09-142-732-81	Sequence 6070, Ap
82	31	100.0	110	2	US-09-513-999C-6070	Sequence 3, Appl
83	31	100.0	125	2	US-09-199-149-3	Sequence 43889, A
84	31	100.0	150	2	US-09-270-767-43889	Sequence 14367, A
85	31	100.0	203	2	US-09-543-661A-4741	Sequence 455, App
86	31	100.0	251	2	US-09-488-039A-14267	Sequence 26, Appl
87	31	100.0	263	2	US-09-303-518D-452	Sequence 1913, A
88	31	100.0	350	2	US-09-913-064A-2	Sequence 7936, Ap
89	31	100.0	392	2	US-09-248-796A-19913	Sequence 2, Appl
90	31	100.0	395	2	US-09-270-767-43336	Sequence 101, App
91	31	100.0	407	2	US-09-949-016-7916	Sequence 124, App
92	31	100.0	438	2	US-09-044-718-2	Sequence 146, App
93	31	100.0	438	2	US-10-062-848-2	Sequence 147, App
94	31	100.0	440	2	US-09-684-855-101	
95	31	100.0	440	2	US-09-684-855-102	
96	31	100.0	440	2	US-09-684-855-124	
97	31	100.0	440	2	US-09-684-855-125	
98	31	100.0	440	2	US-09-684-855-146	
99	31	100.0	440	2	US-09-684-855-147	

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OM protein - protein search, using sw model

Run on: August 21, 2006, 23:40:01 ; Search time 183 Seconds
(without alignments)
12.656 Million cell updates/sec

Title: US-10-766-527-1
Perfect score: 31
Sequence: 1 YGFGG 5

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA Main:*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*\n2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*\n3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*\n4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_PUBCOMB.pep:*\n5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_PUBCOMB.pep:*\n6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	5	US-10-255-679-4	Sequence 4, Appli
2	31	100.0	5	US-10-255-679-6	Sequence 6, Appli
3	31	100.0	5	US-10-255-679-7	Sequence 7, Appli
4	31	100.0	5	US-10-255-679-8	Sequence 8, Appli
5	31	100.0	5	US-10-255-679-9	Sequence 9, Appli
6	31	100.0	5	US-10-255-679-10	Sequence 10, Appli
7	31	100.0	5	US-10-255-679-27	Sequence 27, Appli
8	31	100.0	5	US-10-255-679-32	Sequence 32, Appli
9	31	100.0	5	US-10-255-679-35	Sequence 35, Appli
10	31	100.0	5	US-10-255-679-47	Sequence 47, Appli
11	31	100.0	5	US-10-255-679-48	Sequence 48, Appli
12	31	100.0	5	US-10-255-679-49	Sequence 49, Appli
13	31	100.0	5	US-10-255-679-50	Sequence 50, Appli
14	31	100.0	5	US-10-255-679-51	Sequence 51, Appli
15	31	100.0	5	US-10-255-679-61	Sequence 61, Appli
16	31	100.0	5	US-10-766-527-1	Sequence 1, Appli
17	31	100.0	6	US-10-255-679-38	Sequence 38, Appli
18	31	100.0	6	US-10-255-679-39	Sequence 39, Appli
19	31	100.0	6	US-10-255-679-40	Sequence 40, Appli
20	31	100.0	6	US-10-255-679-41	Sequence 41, Appli
21	31	100.0	6	US-10-255-679-53	Sequence 53, Appli
22	31	100.0	6	US-10-255-679-59	Sequence 59, Appli
23	31	100.0	6	US-10-766-527-4	Sequence 4, Appli
24	31	100.0	14	US-10-255-679-1	Sequence 1, Appli
25	31	100.0	14	US-10-255-679-54	Sequence 54, Appli
26	31	100.0	14	US-10-255-679-55	Sequence 55, Appli
27	31	100.0	14	US-10-068-905-3	Sequence 3, Appli

28	31	100.0	14	US-11-066-697-1237	Sequence 1237, Ap
29	31	100.0	14	US-11-079-632-3	Sequence 3, Appli
30	31	100.0	15	US-10-437-435-13	Sequence 13, Appli
31	31	100.0	47	US-10-425-115-208585	Sequence 208585,
32	31	100.0	61	US-10-425-115-276451	Sequence 276451,
33	31	100.0	62	US-10-425-115-194986	Sequence 194986,
34	31	100.0	62	US-10-425-115-340102	Sequence 340102,
35	31	100.0	63	US-10-425-115-263659	Sequence 263659,
36	31	100.0	63	US-10-425-115-300116	Sequence 300116,
37	31	100.0	63	US-10-425-115-340091	Sequence 340091,
38	31	100.0	63	US-10-425-115-290982	Sequence 290982,
39	31	100.0	73	US-10-425-115-259714	Sequence 259714,
40	31	100.0	79	US-10-425-115-312112	Sequence 312112,
41	31	100.0	82	US-10-425-115-190140	Sequence 190140,
42	31	100.0	83	US-10-425-115-259653	Sequence 259653,
43	31	100.0	84	US-10-424-599-162967	Sequence 162967,
44	31	100.0	90	US-09-864-761-37491	Sequence 37491, A
45	31	100.0	92	US-10-767-701-59845	Sequence 59845, A
46	31	100.0	93	US-10-424-599-159204	Sequence 159204,
47	31	100.0	99	US-10-425-115-259631	Sequence 259631,
48	31	100.0	102	US-10-408-765A-73	Sequence 73, Appli
49	31	100.0	102	US-10-739-930-8447	Sequence 8447, Ap
50	31	100.0	102	US-10-425-115-301864	Sequence 301864,
51	31	100.0	103	US-10-108-605-81	Sequence 81, Appli
52	31	100.0	103	US-10-108-605-159	Sequence 159, App
53	31	100.0	103	US-10-291-307-21	Sequence 21, Appli
54	31	100.0	103	US-10-451-467A-38	Sequence 38, Appli
55	31	100.0	103	US-10-451-467A-324	Sequence 324, App
56	31	100.0	103	US-10-451-467A-682	Sequence 682, App
57	31	100.0	103	US-10-477-369-21	Sequence 21, Appli
58	31	100.0	103	US-10-767-701-47214	Sequence 47214, A
59	31	100.0	103	US-10-767-701-47215	Sequence 47215, A
60	31	100.0	103	US-10-425-115-323722	Sequence 323722,
61	31	100.0	103	US-10-739-930-5693	Sequence 5693, Ap
62	31	100.0	103	US-10-739-930-10425	Sequence 10425, A
63	31	100.0	103	US-10-756-149-4800	Sequence 4800, Ap
64	31	100.0	103	US-10-631-467-731	Sequence 731, App
65	31	100.0	103	US-11-097-143-6348	Sequence 6348, Ap
66	31	100.0	103	US-11-116-959-2	Sequence 2, Appli
67	31	100.0	105	US-10-424-599-145124	Sequence 145124,
68	31	100.0	105	US-10-451-467A-592	Sequence 592, App
69	31	100.0	105	US-10-451-467A-626	Sequence 626, App
70	31	100.0	107	US-10-425-115-340094	Sequence 340094,
71	31	100.0	109	US-10-425-115-191448	Sequence 191448,
72	31	100.0	111	US-10-767-701-54484	Sequence 54484, A
73	31	100.0	111	US-10-739-930-10567	Sequence 10567, A
74	31	100.0	111	US-10-450-763-54484	Sequence 54484, A
75	31	100.0	113	US-10-437-963-132567	Sequence 132567,
76	31	100.0	113	US-10-437-963-181832	Sequence 181832,
77	31	100.0	115	US-10-425-115-272964	Sequence 272964,
78	31	100.0	119	US-10-767-701-47208	Sequence 47208, A
79	31	100.0	120	US-09-925-300-1294	Sequence 1294, Ap
80	31	100.0	121	US-10-425-115-213180	Sequence 213180,
81	31	100.0	123	US-10-739-930-10138	Sequence 10138, A
82	31	100.0	128	US-10-767-701-47217	Sequence 47217, A
83	31	100.0	130	US-10-767-701-47210	Sequence 47210, A
84	31	100.0	132	US-10-424-599-250207	Sequence 250207,
85	31	100.0	133	US-10-029-386-51454	Sequence 51454, A
86	31	100.0	133	US-10-767-701-47213	Sequence 47213, A
87	31	100.0	135	US-10-767-701-47209	Sequence 47209, A
88	31	100.0	137	US-10-424-599-335505	Sequence 335505,
89	31	100.0	139	US-10-767-701-47212	Sequence 47212, A
90	31	100.0	139	US-10-425-115-117346	Sequence 117346,
91	31	100.0	140	US-10-767-701-47211	Sequence 47211, A
92	31	100.0	151	US-10-437-963-190692	Sequence 190692,
93	31	100.0	152	US-10-479-435-5	Sequence 5, Appli
94	31	100.0	159	US-10-424-599-146318	Sequence 146318,
95	31	100.0	159	US-11-087-099-2681	Sequence 2681, Ap
96	31	100.0	165	US-11-079-463-7361	Sequence 7361, Ap
97	31	100.0	165	US-11-079-463-8718	Sequence 8718, Ap
98	31	100.0	181	US-10-425-115-280932	Sequence 280932,
99	31	100.0	185	US-09-988-067B-56	Sequence 56, Appli
100	31	100.0	189	US-11-079-463-7884	Sequence 7884, Ap

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OM protein - protein search, using sw model

Run on: August 21, 2006, 23:40:56 ; Search time 32 Seconds

(without alignments)
10.587 Million cell updates/sec

Title: US-10-766-527-1

Perfect score: 31

Sequence: 1 YGFGG 5

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 243793 seqs, 67754213 residues

Total number of hits satisfying chosen parameters: 243793

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US10_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US11_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US60_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	102	7	US-11-056-355B-11191
2	31	100.0	103	6	US-10-953-349-71
3	31	100.0	103	6	US-10-953-349-2421
4	31	100.0	103	6	US-10-953-349-10509
5	31	100.0	103	6	US-10-953-349-14785
6	31	100.0	103	6	US-10-953-349-15070
7	31	100.0	103	6	US-10-953-349-15185
8	31	100.0	103	6	US-10-953-349-15200
9	31	100.0	103	6	US-10-953-349-15303
10	31	100.0	103	6	US-10-953-349-15371
11	31	100.0	103	6	US-10-953-349-16224
12	31	100.0	103	6	US-10-953-349-18365
13	31	100.0	103	6	US-10-953-349-20454
14	31	100.0	103	6	US-10-953-349-28310
15	31	100.0	103	6	US-10-953-349-28545
16	31	100.0	103	6	US-10-953-349-30550
17	31	100.0	103	6	US-10-953-349-30857
18	31	100.0	103	6	US-10-953-349-35714
19	31	100.0	103	6	US-10-953-349-38640
20	31	100.0	103	6	US-10-953-349-38840
21	31	100.0	103	6	US-10-449-902-29037
22	31	100.0	103	6	US-10-449-902-29097
23	31	100.0	103	6	US-10-449-902-29410
24	31	100.0	103	6	US-10-449-902-29494
25	31	100.0	103	6	US-10-449-902-36925

26	31	100.0	103	7	US-11-105-223-40	Sequence 40, App1
27	31	100.0	103	7	US-11-056-355B-7737	Sequence 7737, App
28	31	100.0	103	7	US-11-056-355B-10506	Sequence 10506, A
29	31	100.0	103	7	US-11-056-355B-15141	Sequence 15141, A
30	31	100.0	103	7	US-11-056-355B-15141	Sequence 15141, A
31	31	100.0	103	7	US-11-056-355B-15141	Sequence 15141, A
32	31	100.0	103	7	US-11-056-355B-20933	Sequence 20933, A
33	31	100.0	103	7	US-11-056-355B-21693	Sequence 21693, A
34	31	100.0	103	7	US-11-056-355B-22100	Sequence 22100, A
35	31	100.0	103	7	US-11-056-355B-26986	Sequence 26986, A
36	31	100.0	103	7	US-11-056-355B-29826	Sequence 29826, A
37	31	100.0	103	7	US-11-056-355B-72011	Sequence 72011, A
38	31	100.0	103	7	US-11-056-355B-73525	Sequence 73525, A
39	31	100.0	103	7	US-11-056-355B-33392	Sequence 33392, A
40	31	100.0	103	7	US-11-056-355B-36429	Sequence 36429, A
41	31	100.0	103	7	US-11-056-355B-84705	Sequence 84705, A
42	31	100.0	103	7	US-11-056-355B-101142	Sequence 101142, A
43	31	100.0	103	7	US-11-056-355B-112381	Sequence 112381, A
44	31	100.0	103	7	US-10-953-349-15184	Sequence 15184, A
45	31	100.0	103	7	US-10-953-349-70	Sequence 70, App1
46	31	100.0	111	7	US-11-056-355B-20534	Sequence 20534, A
47	31	100.0	111	7	US-11-056-355B-72510	Sequence 72510, A
48	31	100.0	113	6	US-10-449-902-38864	Sequence 38864, A
49	31	100.0	116	7	US-11-056-355B-22099	Sequence 22099, A
50	31	100.0	123	7	US-11-056-355B-15140	Sequence 15140, A
51	31	100.0	124	6	US-10-953-349-10508	Sequence 10508, A
52	31	100.0	124	6	US-11-056-355B-21692	Sequence 21692, A
53	31	100.0	125	6	US-10-953-349-15199	Sequence 15199, A
54	31	100.0	127	6	US-10-953-349-14784	Sequence 14784, A
55	31	100.0	127	6	US-10-953-349-15302	Sequence 15302, A
56	31	100.0	127	6	US-10-953-349-20453	Sequence 20453, A
57	31	100.0	127	6	US-10-953-349-28544	Sequence 28544, A
58	31	100.0	128	7	US-11-056-355B-15373	Sequence 15373, A
59	31	100.0	128	6	US-10-953-349-16223	Sequence 16223, A
60	31	100.0	129	6	US-10-953-349-10856	Sequence 10856, A
61	31	100.0	129	6	US-10-953-349-15071	Sequence 15071, A
62	31	100.0	129	6	US-10-953-349-15071	Sequence 15071, A
63	31	100.0	129	6	US-10-953-349-15071	Sequence 15071, A
64	31	100.0	129	6	US-10-953-349-15071	Sequence 15071, A
65	31	100.0	129	6	US-10-953-349-15071	Sequence 15071, A
66	31	100.0	129	6	US-10-953-349-15071	Sequence 15071, A
67	31	100.0	129	6	US-10-953-349-15071	Sequence 15071, A
68	31	100.0	129	6	US-10-953-349-15071	Sequence 15071, A
69	31	100.0	129	6	US-10-953-349-15071	Sequence 15071, A
70	31	100.0	129	6	US-10-953-349-15071	Sequence 15071, A
71	31	100.0	134	6	US-11-056-355B-11190	Sequence 11190, A
72	31	100.0	134	6	US-10-953-349-28309	Sequence 28309, A
73	31	100.0	134	6	US-10-449-902-54526	Sequence 54526, A
74	31	100.0	134	6	US-10-449-902-54526	Sequence 54526, A
75	31	100.0	214	6	US-10-449-902-58835	Sequence 58835, A
76	31	100.0	214	6	US-10-449-902-58835	Sequence 58835, A
77	31	100.0	235	6	US-10-953-349-35009	Sequence 35009, A
78	31	100.0	235	6	US-11-056-355B-35702	Sequence 35702, App
79	31	100.0	235	6	US-11-056-355B-12224	Sequence 12224, App
80	31	100.0	238	6	US-10-953-349-35008	Sequence 35008, A
81	31	100.0	238	6	US-11-056-355B-35711	Sequence 35711, App
82	31	100.0	238	6	US-11-056-355B-12223	Sequence 12223, A
83	31	100.0	248	6	US-10-953-349-28521	Sequence 28521, A
84	31	100.0	248	6	US-11-056-355B-65409	Sequence 65409, A
85	31	100.0	254	7	US-10-953-349-35007	Sequence 35007, A
86	31	100.0	254	7	US-11-056-355B-35707	Sequence 35707, App
87	31	100.0	254	7	US-11-056-355B-12222	Sequence 12222, A
88	31	100.0	307	6	US-10-953-349-28540	Sequence 28540, A
89	31	100.0	307	6	US-10-953-349-28540	Sequence 28540, A
90	31	100.0	308	7	US-11-056-355B-65408	Sequence 65408, A
91	31	100.0	316	6	US-10-471-571A-242	Sequence 242, App
92	31	100.0	317	6	US-10-449-902-77457	Sequence 77457, A
93	31	100.0	322	6	US-10-449-902-29886	Sequence 29886, A
94	31	100.0	334	6	US-11-330-403-8303	Sequence 8303, App
95	31	100.0	338	6	US-10-449-902-11860	Sequence 11860, A
96	31	100.0	343	7	US-11-330-403-16606	Sequence 16606, A
97	31	100.0	346	7	US-11-330-403-9977	Sequence 9977, App
98	31	100.0	347	7	US-11-330-403-18140	Sequence 18140, A

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OM protein - protein search, using sw model

Run on: August 21, 2006, 23:30:51 ; Search time 299 Seconds

(without alignments)
15.468 Million cell updates/sec

Title: US-10-766-527-1

Perfect score: 31

Sequence: 1 YGFG 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 300 summaries

Database :

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	14	P70007_XENLA	P70007 xenopus lae
2	31	100.0	19	Q9N654_DROVI	Q9N654 drosophila
3	31	100.0	19	Q5BM22_RAT	Q5BM22 rattus norv
4	31	100.0	24	P91948_DROVI	P91948 drosophila
5	31	100.0	32	Q7M2K9_RABIT	Q7M2K9 oryctolagus
6	31	100.0	40	Q4YUL1_PLAAB	Q4YUL1 plasmodium
7	31	100.0	45	Q27057_9TRYP	Q27057 trypanosoma
8	31	100.0	55	Q61667_MOUSE	Q61667 mus musculu
9	31	100.0	58	Q7RG24_PLAYO	Q7RG24 plasmodium
10	31	100.0	58	Q38686_ALICE	Q38686 allium cepa
11	31	100.0	65	Q74P21_GEOSL	Q74P21 geobacter s
12	31	100.0	65	Q5WQD5_92Z22	Q5WQD5 uncultured
13	31	100.0	68	Q5WQD6_92Z22	Q5WQD6 uncultured
14	31	100.0	68	Q9U502_MANSE	Q9U502 manduca sex
15	31	100.0	78	Q3SF88_THIDA	Q3SF88 thiodacilla
16	31	100.0	81	Q4IBR9_GIBER	Q4IBR9 gibberella
17	31	100.0	81	Q38Y89_LACSS	Q38Y89 lactobacilli
18	31	100.0	85	Q25800_OVLS	Q25800 ovula arles
19	31	100.0	85	Q50055_SHEEP	Q50055 ovis aries
20	31	100.0	85	Q6R640_CAPIH	Q6R640 capra hircu
21	31	100.0	89	Q4PRB2_BRABR	Q4PRB2 brachydanto
22	31	100.0	92	MLP1_DROME	MLP1 drosophila
23	31	100.0	92	Q6B0K6_9CTUC	Q6B0K6 aptona ger
24	31	100.0	92	Q6XIG1_DROYA	Q6XIG1 drosophila
25	31	100.0	92	Q70080_ANOGA	Q70080 anopheles g
26	31	100.0	93	Q5BF6E_EMENT	Q5BF6E aspergillus
27	31	100.0	94	Q5MGJ0_LONON	Q5MGJ0 lonomia obl
28	31	100.0	94	Q6SA71_BOMMO	Q6SA71 bombyx mori
29	31	100.0	94	Q94412_EPIBL	Q94412 epiblastema sc
30	31	100.0	96	Q3XV68_9PROT	Q3XV68 magnetococc
31	31	100.0	98	Q4TI07_TESTNG	Q4TI07 tetradodon n

32	31	100.0	102	1	H41_ASHCO	Q757k0 ashyia goes
33	31	100.0	102	1	H41_EMENT	P23750 emeticella
34	31	100.0	102	1	H41_PENFN	Q711m0 penicillium
35	31	100.0	102	1	H41_TETPY	P02310 tetranymena
36	31	100.0	102	1	H41_WHAT	P62785 triticum ae
37	31	100.0	102	1	H42_ASHCO	Q75ax1 ashyia goes
38	31	100.0	102	1	H42_EMENT	P23751 emeticella
39	31	100.0	102	1	H42_PENFN	Q8n1q8 penicillium
40	31	100.0	102	1	H42_TETPY	P69151 tetranymena
41	31	100.0	102	1	H42_TETTH	P69152 tetranymena
42	31	100.0	102	1	H43_WHEAT	P62786 triticum ae
43	31	100.0	102	1	H43_WHAIZ	Q41811 zea mays (m
44	31	100.0	102	1	H48_CHICK	P70081 gallus gall
45	31	100.0	102	1	H4_ACRAS	P84048 acrolopiops
46	31	100.0	102	1	H4_ACRFO	P35059 acropora fo
47	31	100.0	102	1	H4_APIME	Q27443 ascaris suu
48	31	100.0	102	1	H4_APICA	Q8nctv8 aplysia cal
49	31	100.0	102	1	H4_ARATH	P59259 arabidopsis
50	31	100.0	102	1	H4_ARXAD	Q8j1l3 arxula aden
51	31	100.0	102	1	H4_ASCSU	P84047 asellus aqu
52	31	100.0	102	1	H4_ASEBAQ	Q71Kt3 aspergillus
53	31	100.0	102	1	H4_ASPFU	Q7cmu7 aspergillus
54	31	100.0	102	1	H4_ASPOR	P62803 bos taurus
55	31	100.0	102	1	H4_BOVIN	P62784 caenothabdi
56	31	100.0	102	1	H4_CABEL	P62800 caltrina mos
57	31	100.0	102	1	H4_CAIMO	Q8n1g3 candida gla
58	31	100.0	102	1	H4_CANGA	Q71v09 capsicum an
59	31	100.0	102	1	H4_CAPAN	Q7kqd1 chaetopteru
60	31	100.0	102	1	H4_CHAVR	Q6pm15 chelidonium
61	31	100.0	102	1	H4_CHBMT	P62801 gallus gall
62	31	100.0	102	1	H4_CHICK	P84046 chironomus
63	31	100.0	102	1	H4_CHITH	P84046 chlamydomon
64	31	100.0	102	1	H4_CHLRE	Q61af1 dendronephr
65	31	100.0	102	1	H4_DENKL	P91882 diadromus p
66	31	100.0	102	1	H4_DIAPU	P84041 drosophila
67	31	100.0	102	1	H4_DROBR	P84042 drosophila
68	31	100.0	102	1	H4_DROHY	Q761e7 drosophila
69	31	100.0	102	1	H4_DROMA	P84040 drosophila
70	31	100.0	102	1	H4_DROME	Q76ef1 drosophila
71	31	100.0	102	1	H4_DROOR	P84043 drosophila
72	31	100.0	102	1	H4_DROSE	Q761e5 drosophila
73	31	100.0	102	1	H4_DROSI	P84044 drosophila
74	31	100.0	102	1	H4_DROTE	Q87718 elmeria ten
75	31	100.0	102	1	H4_DROYA	Q6z8t3 eucalyptus
76	31	100.0	102	1	H4_EIMTE	Q61af3 flavaria tr
77	31	100.0	102	1	H4_RUCGL	P62776 holoturia
78	31	100.0	102	1	H4_PLATR	P62805 homo sapien
79	31	100.0	102	1	H4_HOLTV	P62887 lolium temu
80	31	100.0	102	1	H4_HUMAN	P35057 lycopersico
81	31	100.0	102	1	H4_LOLTE	P62782 lytechinus
82	31	100.0	102	1	H4_LYCES	P62787 zea mays (m
83	31	100.0	102	1	H4_LYTPI	Q9nd15 mortierella
84	31	100.0	102	1	H4_MAIZS	P62806 mus musculu
85	31	100.0	102	1	H4_MORAP	P84045 myrmica rug
86	31	100.0	102	1	H4_MOUSE	Q6v773 mytilus cal
87	31	100.0	102	1	H4_MYRRU	Q6v774 mytilus edu
88	31	100.0	102	1	H4_MYTCA	Q786c0 mytilus gal
89	31	100.0	102	1	H4_MYTCH	Q6v790 mytilus tro
90	31	100.0	102	1	H4_MYTED	P04914 neurospora
91	31	100.0	102	1	H4_MYTGA	P82888 olisthodisc
92	31	100.0	102	1	H4_MYTGR	P62797 oncorhynch
93	31	100.0	102	1	H4_NEUCR	P62796 oreochromis
94	31	100.0	102	1	H4_OILIU	P62780 paracentroc
95	31	100.0	102	1	H4_ONCMY	P62788 pismu sativ
96	31	100.0	102	1	H4_ORENT	P04915 physarum po
97	31	100.0	102	1	H4_PARKI	P62802 sus scrofa
98	31	100.0	102	1	H4_PEA	P62777 pisaaster br
99	31	100.0	102	1	H4_PHPPO	P62778 pisaaster oc
100	31	100.0	102	1	H4_PIG	P62795 platyneureis
101	31	100.0	102	1	H4_PISBR	P62781 psammochinu
102	31	100.0	102	1	H4_PISOC	
103	31	100.0	102	1	H4_PLADU	
104	31	100.0	102	1	H4_PSAMI	

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OM protein - protein search, using sw model

Run on: February 17, 2005, 19:19:55 ; Search time 61 Seconds
(without alignments)
31.702 Million cell updates/sec

Title: **31**
Perfect score: **31**
Sequence: 1 YGFGG 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 716780

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 200 summaries

Database : A-Geneseq_1Dec04:*

1: **31** geneseqp19808:*
2: geneseqp19808:*
3: geneseqp19808:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	31	100.0	5 2	AAR76124 Osteogeni
2	31	100.0	5 2	ADC73222 Cyclic ps
3	31	100.0	5 6	ABP72525 Osteogeni
4	31	100.0	6 2	AAR62388 Osteoblas
5	31	100.0	6 2	AAR62954 Osteogeni
6	31	100.0	6 2	ADC73230 Cyclic ps
7	31	100.0	6 2	ADC73233 Cyclic ps
8	31	100.0	6 2	ADC73229 Cyclic ps
9	31	100.0	6 6	ABP72528 Osteogeni
10	31	100.0	14 2	AAR06551 Osteogeni
11	31	100.0	14 2	AAR43890 Osteogeni
12	31	100.0	14 2	AAR43888 Osteogeni
13	31	100.0	14 2	AAR62952 Osteogeni
14	31	100.0	14 4	AA92061 Growth fa
15	31	100.0	14 6	ABR63887 Osteogeni
16	31	100.0	14 6	ADA27392 Osteogeni
17	31	100.0	14 8	ADL35204 Human OGP
18	31	100.0	15 2	AAR43889 Osteogeni
19	31	100.0	17 2	AAR48440 Histogran
20	31	100.0	17 2	AAR48449 Histogran
21	31	100.0	17 2	AAR48442 Histogran
22	31	100.0	17 2	AAR48448 Histogran
23	31	100.0	17 2	AAR48444 Histogran
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OM protein - protein search, using sw model

Run on: February 17, 2005, 19:28:36 / Search time 18 Seconds
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Title: **US-10-766-527-1**
Perfect score: 31
Sequence: 1 YGFCG 5

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 196327

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 200 summaries

Database: **igene6.patent.us**

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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OM protein - protein search, using BW model

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OM protein - protein search, using SW model

Run on: February 17, 2005, 19:27:01 ; Search time 11.25 Seconds

(without alignments)
42.763 Million cell updates/sec

Title: ~~US-10-766-527-1~~

Perfect score: 3.1

Sequence: 1 YGFGG 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3886

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	14	2 I51432	histone H4-1 prenu
2	31	100.0	18	2 C30309	histone H4 - Bupio
3	25	80.6	16	2 A47393	neuropeptide calla
4	24	77.4	14	2 A17150	glucose 1-dehydrog
5	23	74.2	13	2 A33933	Ig kappa chain J r
6	22	71.0	10	2 C45474	thrombospondin 2 -
7	22	71.0	17	2 S33609	extensin - maize (
8	22	71.0	20	2 PH1341	Ig heavy chain Df
9	21	67.7	10	2 F60527	sperm-activating p
10	21	67.7	14	2 B33098	21k exoantigen (v
11	21	67.7	15	2 PC4269	unidentified OR310
12	21	67.7	20	2 A61525	alpha-lactalbumin
13	20	64.5	18	2 S20322	gluten - wheat
14	19	61.3	7	1 A61324	dermorphin - Rohde
15	19	61.3	7	2 S36662	dermorphin (lys-7)
16	19	61.3	8	2 D47393	neuropeptide calla
17	19	61.3	10	2 A60589	sperm-activating p
18	19	61.3	13	2 S48210	collagen alpha 1(V
19	19	61.3	15	2 B56978	collagen alpha 2(X
20	19	61.3	16	2 T44936	calmodulin kinase
21	19	61.3	17	2 S09085	microsomal chain 4
22	19	61.3	20	2 P50087	T-cell receptor be
23	18	58.1	4	2 A53284	180X exoantigen -
24	18	58.1	7	2 H33098	T-cell receptor be
25	18	58.1	7	2 PT0725	T-cell receptor be
26	18	58.1	8	2 E47393	neuropeptide calla
27	18	58.1	8	2 PC4373	telomeric and telr
28	18	58.1	8	2 D24180	fibrinogen beta ch
29	18	58.1	9	2 D24180	fibrinogen beta ch

30	18	58.1	9	2 F28854	fibrinopeptide B -
31	18	58.1	9	2 PT0225	Ig heavy chain CDR
32	18	58.1	9	2 S10784	enamelin I - bovin
33	18	58.1	9	2 PC7074	translation elonga
34	18	58.1	10	2 PT0632	T-cell receptor be
35	18	58.1	10	2 PT0664	T-cell receptor be
36	18	58.1	10	2 S06964	hypothetical prote
37	18	58.1	10	2 B60589	sperm-activating p
38	18	58.1	11	2 A44755	20alpha-hydroxyste
39	18	58.1	12	2 A49261	coagulation factor
40	18	58.1	12	2 A58375	microcin B17 - Bac
41	18	58.1	12	2 PT0263	Ig heavy chain CRD
42	18	58.1	13	2 B20907	Ig kappa-1 chain J
43	18	58.1	13	2 B26406	Ig kappa chain J r
44	18	58.1	13	2 S22761	Ig lambda-2 chain
45	18	58.1	13	2 A47630	Ig kappa chain J r
46	18	58.1	13	2 PS0277	glyceroldehyde-3-p
47	18	58.1	14	2 PH0747	T-cell receptor be
48	18	58.1	15	2 A26228	spot 42 protein -
49	18	58.1	15	2 J70610	leukocyte chemoat
50	18	58.1	16	2 A12729	glutamate dehydrog
51	18	58.1	16	2 S11805	heat shock protein
52	18	58.1	16	2 A29520	amino-acid racemas
53	18	58.1	18	2 B32473	histidine-rich pro
54	18	58.1	18	2 PH1792	T-cell receptor al
55	18	58.1	18	2 S47196	T-cell receptor J-
56	18	58.1	18	2 S40502	20-alpha-hydroxyst
57	18	58.1	19	2 A28814	Ig kappa chain V r
58	18	58.1	19	2 A39504	octamer-binding pr
59	18	58.1	19	2 S68393	H+-transporting tw
60	18	58.1	19	2 S74087	antibacterial prot
61	18	58.1	19	2 B48138	d(TTACGG)n-binding
62	18	58.1	20	2 S17501	glutaminase - Alca
63	18	58.1	20	2 PH0115	protein QR200034 -
64	17	54.8	8	2 PH1618	Ig H chain V-D-J r
65	17	54.8	12	2 S26548	T-cell receptor be
66	17	54.8	12	2 S26544	T-cell receptor be
67	17	54.8	12	2 S26547	T-cell receptor be
68	17	54.8	12	2 S26546	T-cell receptor be
69	17	54.8	12	2 S26541	T-cell receptor be
70	17	54.8	12	2 PH1458	T-cell receptor be
71	17	54.8	12	2 PH1462	T-cell receptor be
72	17	54.8	12	2 PH1461	T-cell receptor be
73	17	54.8	12	2 PH1457	T-cell receptor be
74	17	54.8	12	2 PH1459	T-cell receptor be
75	17	54.8	13	2 C47630	Ig kappa chain J r
76	17	54.8	14	2 S23639	Ig kappa chain J s
77	17	54.8	14	2 A32654	fibrinopeptide A -
78	17	54.8	15	2 H56978	collagen alpha 1(X
79	17	54.8	16	1 MTDPBS	melanotropin beta
80	17	54.8	16	2 S57517	T cell receptor be
81	17	54.8	16	2 C49048	T-cell receptor be
82	17	54.8	16	2 PH1473	T-cell receptor be
83	17	54.8	16	2 S28433	major outer membra
84	17	54.8	17	2 H49048	T-cell receptor be
85	17	54.8	17	2 T49048	T-cell receptor be
86	17	54.8	17	2 PH1367	Ig heavy chain DJ
87	17	54.8	17	2 T67324	CD33 antigen homol
88	17	54.8	18	2 PH1323	Ig heavy chain DJ
89	17	54.8	18	2 B49048	T-cell receptor be
90	17	54.8	18	2 PQ0072	T-cell receptor be
91	17	54.8	18	2 B48839	T-cell receptor be
92	17	54.8	19	2 A44379	alpha-conotoxin SI
93	17	54.8	19	2 G49048	T-cell receptor be
94	17	54.8	19	2 PT0332	Ig heavy chain CRD
95	17	54.8	19	2 E49048	T-cell receptor be
96	17	54.8	19	2 PS0332	phospholipase A2 (
97	17	54.8	20	2 F49048	T-cell receptor be
98	17	54.8	20	2 A49048	T-cell receptor be
99	17	54.8	20	2 B61577	17.6k serine prote
100	17	54.8	20	2 A54042	mannose-6-phosphat
101	17	54.8	20	2 A60801	actosome stabilizi
102	16	51.6	2	2 C53284	T-cell receptor be

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OM protein - protein search, using sw model

Run on: February 17, 2005, 19:26:05 ; Search time 77.5 Seconds
(without alignments)
33.037 Million cell updates/sec

Title: us-10-766-527-1
Perfect score: 31
Sequence: 1 YGFCG 5

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 segs, 512079187 residues

Total number of hits satisfying chosen parameters: 12050

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database :

1: ~~uniprot_sprot~~:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	31	100.0	14 2 P70007	P70007 xenopus lae
2	31	100.0	19 2 Q9N654	Q9N654 drosophila
3	25	80.6	16 1 AL11_CALVO	P41839 calliphora
4	24	77.4	19 2 Q85671	Q85671 recivitus ty
5	24	77.4	20 1 KORC_METTM	P80906 mechanobact
6	24	77.4	20 2 Q85670	Q85670 recivitus ty
7	23	74.2	11 2 Q70Y64	Q70Y64 plectranthu
8	23	74.2	17 2 Q6EX59	Q6EX59 thymus serp
9	23	74.2	17 2 Q9QV41	Q9QV41 mus sp. . s
10	22	71.0	11 2 Q9TWM2	Q9TWM2 aplysia cal
11	22	71.0	17 2 Q9S857	Q9S857 zea.mays (m
12	22	71.0	19 2 Q6LDN4	Q6LDN4 rhodobacter
13	21	67.7	10 1 CU30_LOCM1	P11735 locustra.mig
14	21	67.7	10 2 Q7M379	Q7M379 tripanesetes
15	21	67.7	14 2 Q86922	Q86922 human cytom
16	21	67.7	20 2 Q9TRC0	Q9TRC0 bos taurus
17	20	64.5	13 2 Q9UDR0	Q9UDR0 homo sapien
18	20	64.5	17 2 Q9TR22	Q9TR22 bos taurus
19	20	64.5	18 2 Q7M1G0	Q7M1G0 triticum ae
20	19	61.3	5 1 AL14_CARMA	P81817 carcinius ma
21	19	61.3	7 1 AL12_CARMA	P81805 carcinius ma
22	19	61.3	7 1 AL13_CARMA	P81806 carcinius ma
23	19	61.3	7 1 AL14_CARMA	P81808 carcinius ma
24	19	61.3	7 1 AL15_CARMA	P81810 carcinius ma
25	19	61.3	8 1 AL15_CARMA	P81815 carcinius ma
26	19	61.3	8 1 AL17_CARMA	P81818 carcinius ma
27	19	61.3	8 1 AL17_CARMA	P81820 carcinius ma
28	19	61.3	8 1 AL18_CARMA	P81821 carcinius ma
29	19	61.3	8 1 AL11_CYDPO	P82152 cydia pomon
30	19	61.3	8 1 AL14_CYDPO	P82154 cydia pomon
31	19	61.3	8 1 AL14_CALVO	P41840 calliphora